☐ **1:** I39311. Kruppel-type zinc...[gi:2136376] BLink, Domains, Links

```
LOCUS       I39311                  572 aa            linear   PRI 01-DEC-2000
DEFINITION  Kruppel-type zinc finger protein ZNF74 - human.
ACCESSION   I39311
VERSION     I39311  GI:2136376
DBSOURCE    pir: locus I39311;

            summary: #length 572 #molecular-weight 64193 #checksum 1376
            ;
            superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat
            homology
            ;
            PIR dates: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
            01-Dec-2000
            .
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (residues 1 to 572)
  AUTHORS   Aubry,M., Marineau,C., Zhang,F.R., Zahed,L., Figlewicz,D.,
            Delattre,O., Thomas,G., de Jong,P.J., Julien,J.P. and Rouleau,G.A.
  TITLE     Cloning of six new genes with zinc finger motifs mapping to short
            and long arms of human acrocentric chromosome 22 (p and q11.2)
  JOURNAL   Genomics 13 (3), 641-648 (1992)
  MEDLINE   92347859
   PUBMED   1639391
REFERENCE   2  (residues 1 to 572)
  AUTHORS   Aubry,M., Demczuk,S., Desmaze,C., Aikem,M., Aurias,A., Julien,J.P.
            and Rouleau,G.A.
  TITLE     Isolation of a zinc finger gene consistently deleted in DiGeorge
            syndrome
  JOURNAL   Hum. Mol. Genet. 2 (10), 1583-1587 (1993)
  MEDLINE   94093543
   PUBMED   8268910
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     Protein         1..572
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      121 eggplldtrk nvqategrtk aparlcagen astpsepekf pqvrrqrgag agegefvcge
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      241 fschsslnvh qrihtgerpy kcsacekafs cssllsmhlr vhtgekpyrc gecgkafnqr
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      361 lhqrthtgek pfkcadcgkg fschayllvh rrihsgekpf kcnecgkafs shaylivhrr
      421 ihtgekpfdc sqcwkafsch sslimhqrih tgekpykcse cgrafsqnhc likhqkihsg
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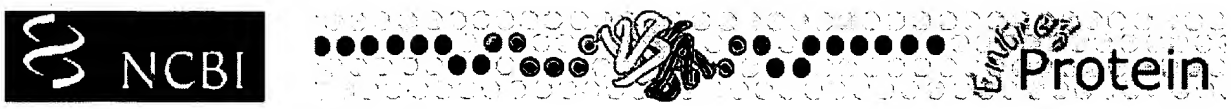

☐ 1: 1K5JE. Chain E, The Crys...[gi:16974926] BLink, Domains, Links

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LOCUS       1K5J_E                    124 aa            linear   VRT 10-OCT-2001
DEFINITION  Chain E, The Crystal Structure Of Nucleoplasmin-Core.
ACCESSION   1K5J_E
VERSION     1K5J_E  GI:16974926
DBSOURCE    pdb: molecule 1K5J, chain 69, release Oct 10, 2001;
            deposition: Oct 10, 2001;
            class: Chaperone;
            source: Mol_id: 1; Organism_scientific: Xenopus Laevis; Gene:
            Nucleoplasmin; Expression_system: Escherichia Coli;
            Expression_system_common: Bacteria; Expression_system_strain:
            Bl21(De3); Expression_system_vector_type: Plasmid;
            Expression_system_plasmid: Prk172;
            Exp. method: X-Ray Diffraction.
KEYWORDS    .
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus.
REFERENCE   1  (residues 1 to 124)
  AUTHORS   Dutta,S., Akey,I.V., Dingwall,C., Hartman,K.L., Laue,T.,
            Nolte,R.T., Head,J.F. and Akey,C.W.
  TITLE     The crystal structure of nucleoplasmin-core: implications for
            histone binding and nucleosome assembly
  JOURNAL   Mol. Cell 8 (4), 841-853 (2001)
  MEDLINE   21541925
   PUBMED   11684019
REFERENCE   2  (residues 1 to 124)
  AUTHORS   Dutta,S., Akey,I.V., Dingwall,C., Hartman,K.L., Laue,T.,
            Nolte,R.T., Head,J.F. and Akey,C.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-OCT-2001)
COMMENT     Revision History:
            NOV 21 1 Typographical
            NOV 1 1 Initial Entry.
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     SecStr          110..118
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      121 ēēdy
//
```


h cb h g e e e fcg c e e e b e

CORRECTIONS AND CLARIFICATIONS

RESEARCH ARTICLES: "Delineation of mRNA export pathways by the use of cell-permeable peptides" by I.-E. Gallouzi and J. A. Steitz (30 Nov. 2001, p. 1895). The sequences of several of the peptides used were reported incorrectly in Fig. 1A. The actual amino acid sequences that were conjugated to AP are as follows, with substitutions indicated in bold, additions denoted by underlining, and positions of amino acids not present in the peptides used indicated by [-]: HNS: RRFGGPVHHQAQRFRFSPMGVDHMSG**L**SGVNVPG; NES: [-]QLPPLERLTLD; mNES: [-]QLPP**DL**RL**T**LD; and M9: NNQSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQ[---]. It has been verified that the substitution of L for I [I is present in the HNS sequence of HuR; X. C. Fan, J. A. Steitz, *Proc. Natl. Acad. Sci. U.S.A.* **95**, 15293 (1998)] does not alter the activity of the AP-HNS in the heterokaryon shuttling assay. Similarly, the absence of NH_2-terminal N and presence of COOH-terminal GGY (as in hnRNP A1) does not alter the activity of AP-M9. The mNES sequence used and reported above is that of the well-characterized NES mutation called M10 [M. H. Malim, S. Bohnlein, J. Hauber, B. R. Cullen, *Cell* **58**, 205 (1989)]; like the misrecorded mNES sequence, it differs from NES in only two amino acids. The scHNS and scM9 sequences originally reported are scrambled versions of the correct HNS and M9 sequences. Nicholas K. Conrad and Angie S. Grech are acknowledged for their work in discovering the errors and repeating the experiments.